

STIC Search Report Biotech-Chem Library

SIO Defendence in the control of the

TO: Mark Shibuya

Location: REM-2A10&2C18

Art Unit: 1639

Monday, August 01, 2005

Case Serial Number: 09/667237

From: Edward Hart

Location: Biotech-Chem Library

REM-1A55

Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Shibuya,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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From:

Sent:

To:

Subject:

Shibuya, Mark Wednesday, July 27, 2005 2:30 PM STIC-Biotech/ChemLib Search req. for SEQ NO:12 of 09/667,237.

Please search SEQ NO:12 of 09/667,237.

This case is before the first action on the merits.

Mark Shibuya Art Unit 1639, Remsen 2a10, ext: 2-0806

Туре	of Search
^	
NA#:	AA#:
Interference	: SPDI:
S/L:	Oligomer:
Encode/Tran	nsl:
Structure#:	Text:
Inventor:	Litigation:

******* Vendors and cost where applicable STN:_ DIALOG:____ QUESTEL/ORBIT:__ LEXIS/NEXIS:_ SEQUENCE SYSTEM: WWW/Internet: Other(Specify):

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STIC SEARCH RESULTS FEEDBACK FORM

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	CUI		173	Ш			

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

VO	lulitary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
×	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	☐ Helped examiner better understand the invention.
	☐ Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



Results were not useful in determining patentability or understanding the invention.

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Aug

Mon

RESULT

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Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                             Rattus.
       RESULT 7
AC126150/c
                                                                                                                                                                                                                                 ORGANISM
                                                                              DEFINITION
                                                                                                                            ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
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JOURNAL
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TITLE
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                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems; such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw.; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Lebratish pUC subclones occasionally display inconsistency over the length of monouncleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                               26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-202A10 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                     øsanger.ac.uk
820884.
                                                       nkage group
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                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-FEB-2004) Wellcome Trust Sanger Institu
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest
On Feb 26, 2004 this sequence version replaced gi:42
                              BX470087

218404 bp DNA linear

Zebrafish DNA sequence from clone CH211-202A10 in li
                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata;
pterygii; Teleostei; Ostariophysi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Danio rerio"
/wol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-202A10"
/clone_lib="CHORI-211"
                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Cra
Actinopterygii, Neopterygii, Tele
Cypriniformes, Cyprinidae, Danio
1 (bages 1 to 218404)
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                                                                                                                             GI:43823873
                                                                                                                                                                               Danio rerio (zebrafish)
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                                                                            complete sequence
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BX470087.8
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Best Local &
BX470087/c
                                                    DEFINITION
                                                                                                                                                                                                      ORGANISM
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AUTHORS
                                                                                                      ACCESSION
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                                                                                                                            VERSION
KEYWORDS
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Saftus.

Rattus.

Rattus.

Rattus.

Rattus.

Ruzny, D.Marie., Matker, M.Lee., Abramzon, S., Adams, C., Alder, J., Alder, C., Allan, H., Alabrooks, S., Amin, A., Anguiano, D., Alder, J., Alder, C., Allan, H., Alabrooks, S., Amin, A., Anguiano, D., Alder, J., Alder, J., Alder, J., Algarder, B., Barber, M., Barnstead, M., Benahmed, F., Balddhin, D., Banderanaike, D., Barber, M., Barnstead, M., Benahmed, F., Bryant, N., Barnstead, M., Benahmed, F., Chader, J., Chaderon, B., Chaderon, B., Chader, J., Labow, H., Levan, J., Levan, J., Levan, J., Labow, H., Levan, J., Levan, J., Labow, H., Levan, J., Levan, J., Labow, H., Levan, J., Labow, H., Labor, J.,
                   HTG 13-MAY-2003
IN PROGRESS
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                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                       Craniata, Vertebrata; Euteleost
Sciurognathi; Muridae; Murinae;
                     linear
SEQUENCING
                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat) Rattus norvegicus
                     DNA
Rattus norvegicus clone CH230-69L10, ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                      GI:30580907
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to 241173)
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(bases 1

REFERENCE

STS 15-OCT-2003

sequence

4

-667-237b-12.rge

ტ 0 -

18

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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/map="7-144325-144544-AC087063.20.1.241381"
/clone_lib="Roche Palo Alto"
/note="SNPs developed from assay sequences derived from 15 different strains-of mice (as of October 1, 2003). Those strains include A/J, A/HeJ, -129/Sv, AKR/J, B10.D2-H2/oSnJ, BALB/cByJ, BALB/cJ, C3H/HeJ, C57BL/6J,~CAST/Ei, DBA/2J, MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.~"
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2 in independent field
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 402)
Usuka, J., Liao, G., Cheng, J., Nguyen, A., Bach, C., Puech, A., McPherson, J.D., Foernzler, D. and Peltz, G.
Mus musculus SNPs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA linear INV 15-MAR-3 from Solomon Islands merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum (malaria parasite P. falciparum)

Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 410)

Eisen, D.P., Cloonan, N., Baddeley, A., Eri, R. and Saul, A.

Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent fiestsolates of Plasmodium falciparum

Unpublished

2 (bases 1 to 410)

Eisen, D.P., Cloonan, N., Baddeley, A., Eri, R. and Saul, A.

Direct Submission

Chaptial, Herston Rd., Herston, QLD 4029, Australia
                                                                     ONA linear STS 1:
musculus STS genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palo Alto, CA 94024,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Jonathan Usuka
Roche Palo Alto
Roche Palo Alto
3431 Hillview Ave, Mailstop S3-1, Palo Alto, CA STel: 6508555807
Email: Jonathan.Usuka@roche.com
Primer A: No primer submitted
Primer B: No primer submitted.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
2
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larity 86.8%; Pred. No. 6.6;
Conservative 0; Mismatches
                                                                          DNA
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                                                                                                 Mus
                                                                    BV090840
RPAMMSEQ0002739 Roche Palo Alto Mutagged site.
BV090840
BV090840.1 GI:37668319
STS.
Mus musculus (house mouse)
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surface protein 2 gene, partial
AF329581
AF329581.1 GI:13345560
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les 33; Conser
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Best Local S
Matches 33
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KEYWORDS
SOURCE
                              RESULT 8
BV090840
LOCUS
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KEYWORDS
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Sat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23268918.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                               separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        estimation
igs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project Information.

Center project name: GIWC

Center clone name: CH230-69L10

----- Summary Statistics
Assembly program: Atlas 3.0;

Consensus quality: 213355 bases at least Q30

Consensus quality: 219597 bases at least Q20

Consensus quality: 223913 bases at least Q20

Consensus quality: 223913 bases at least Q20

Estimated insert size: 225595; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GIWC
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|mol_type="genomic DNA"
|db_xref="taxon:10116"
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larity 87.2%; Pred. No.
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/note="wgs_contig"
101829. .103618
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/note="wgs_contig"
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/note="wgs_
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/note="wgs_
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/note="tissue-specific transcript"
join(<289. .315,1107. .1136,3194. .3226,4880. .>4912)
/géne="Crpd"
/note="CRP1 domain; SRCR family member; CRP-ductin;
ebnerin; dmbt1; hensin; vomeroglandin"
/codon_start=3
/product="muclin"
/product="muclin"
/protein_id="AAF93167.1"
/db_xref="GI:9739246"
/translation="SQTSSPTPGWWNPGGTNNDVFYPTEQTTAEQTTIPDYTPI
                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina
1 (bases 1 to 5460)
Boulatnikov, I. and De Lisle, R.C.
Binding of the Golgi Sorting Receptor Muclin to Pancreatic
through Sulfated O-linked Oligosaccharides
J. Biol. Chem. 279 (39), 40918-40926 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 5460)
De Lisle, R.C. and Ziemer, D.
Direct Submission
Submitted (04-JUL-2000) Anatomy & Cell Biology, University
Kansas Medical Center, 3901 Rainbow Blvd., Kansas City, KS
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Pred. No. 5.5;
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313 from Patent WO2004074320
                                                     Score 30; DB 3
Pred. No. 6.5;
0; Mismatches
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1. .5460
/organism="Mus musculus"
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/db_xref="taxon:10090"
<289. .>4912
/gene="Crpd"
join(<289. .315,1107. .113
                                                                                                                                                                                                         AY004216
Mus musculus muclin (Crpd) gene,
AY004216
AY004216.1 GI:9739245
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ilarity 86.8%;
Conservative
                                                    Query Match
Best Local Similarity 86.8%;
Matches 33; Conservative
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Matches 33; Conser
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CQ869892
CQ869892.1
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DEFINITION
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasme
1 (bases 1 to 558)
Felger, I., Steiger, S., Hatz, C., Smith, T. and Beck, H.-P
Antigenic cross-reactivity between different alleles of
Plasmodium falciparum merozoite surface protein 2
Parasite Immunol. 25 (11-12), 531-543 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Felger, I:
Direct Submission
Submitted (28-AUG-2003) MPI, Swiss Tropical Institute,
S7, Basel CH-4002, Switzerland
Location/Qualifiers
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Plasmodium falciparum merozoite surface protein msp2-B allele, partial cds.
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Plasmodium falciparum"
/mol_type="genomic DNA"
/db_xref="taxon:5833"
/chromosome="2"
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Pred. No. 6.6;
0; Mismatches
                                                                           /country="Solomon Islands"
/note="genotype: 3"
<1. .>410
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Location/Qualifiers
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/gene="msp2"
/allele="B"
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/gene="msp2"
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ilarity 86.8%;
Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                      and Malandro, M.S
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                                                                                                                                                Morris, D.W., Morris, D.W. and Malandro, M. (Novel therapeutic targets in cancer Patent: WO 2004074320-A 313 02-SEP-2004; Sagres Discovery, Inc. (US) Location/Qualifiers
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Rattus norvegicus clone CH230-228G24,
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                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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HTG; HTGS PHASE1; HTGS DRAFT;
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Pred.
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86.8%;
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                                                Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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AC117361
                           musculus
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Best Local Similarity
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                   Mus
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AC117361/c
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ORGANISM
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AUTHORS
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23194821.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', within each contig-scaffold', individual sequence contigs are ordered and oriented, and sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Waillson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
Worley, K.C.
Direct Submission
Submitted (10-APR-2002) Human Genome Sequencing Center, Department Submitted (10-APR-2002) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111630: contig of 111630 bp in length
111730: gap of unknown length
201448: contig of 89718 bp in length
201548: gap of unknown length
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/lor College of Medicine
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Center code: BCM
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Unpublished
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FEATURES

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Interpretation of the control of the
the linear HTG 15-NOV-2002
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Rattus norvegicus clone CH230-123D20, *** SEQUENCING IN PROGRESS
***, 5 unordered pieces.
AC117014
AC1
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Pred. No. 4.3;
); Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="rp23-20047"
clone_lib="RPCI -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Local Similarity 86.8%;
nes 33; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .241381
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                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
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AC117014
LOCUS
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Matches
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                                                                                                                                                                                                                                                                                                                     COMMENT
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2 (bases 1 to 241381)

Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.

Direct Submission

Submitted (02-DEC-2000) Department Of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA

3 (bases 1 to 241381)

Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.

Direct Submission

Submitted (14-JUL-2002) Department Of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA
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4 (bases 1 to 241381)
Wu,H., Hu,P., Yang,L., Prescott,A., DeLisle,B. and Roe,B.A.
Direct Submission
Submitted (16-JUL-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Murinae; Mus
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om 208, Norman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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5 (bases 1 to 241381)
Wu,H., Hu,P., Yang,L., Prescott,A., DeLisle,B. and Roe,B.A.
Direct Submission
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Wu,H., Hu,P., Yang,L., Prescott,A., DeLisle,B. and Roms musculus BAC Clone rp23-20047
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       1549 202550: contig of 1002 bp in length 202650: gap of unknown length 203739: contig of 1089 bp in length. Location/Qualifiers

1. .203739

/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-228G24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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The University Of Oklahoma, 620 Parrington Oval,
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang, L., Prescott, A., DeLisle, B.
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Pred. No. 4.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                            109021. .111630
/note="wgs_contig"
171475. .172939
/note="wgs_contig"
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6 (bases 1 to 241381)
Wu,H., Hu,P., Yang,L.,
Direct Submission
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ilarity 86.8%;
Conservative
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Submission
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AC087063.20
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202551
202651
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Best Local
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DEFINITION

RESULT 14 AC087063

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Matches

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL REFERENCE

TITLE

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JOURNAL

REFERENCE AUTHORS TITLE

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AUTHORS TITLE

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us-09-667-237b-12.rg

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Worley, K.C.

Worley, K.C.

Direct Submission

Submitted (06-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Exat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23267317.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, B., Mayua, P., Martin, K., Martinez, E.,
Mangum, B., Mated, M.P., McNeill, T.Z., Menen, E.,
Milosavijevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
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Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L. L.,
Pasternak, S., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shateman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Sneed, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usanai, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B.,
Williams, G., Willson, R., Wu, J., Yakub, S., Yen, J., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Lupublished
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: GTLL
Center clone name: GTLL
Center clone name: GTLL
Center clone name: GTLL
Center clone name: GTLL
Center project name: GTLL
Assembly program: Phrap; version 0.990329
Consensus quality: 218498 bases at least Q30
Consensus quality: 221512 bases at least Q20
Estimated insert size: 220593; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------ Genome Center
Center: Baylor College of Medicine
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REFERENCE
AUTHORS
TITLE
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COMMENT

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Gaps
                                                     the accession number will
arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                1 7122: contig of 7122 bp in length 7222: gap of unknown length 7222: gap of unknown length 1394 236493: gap of unknown length 1394 239610: contig of 3117 bp in length 1511 239710: gap of unknown length 1511 254301: contig of 14591 bp in length 1302 254401: gap of unknown length 1502 255613: contig of 1212 bp in length 1602 255613: contig of 1212 bp in length 16055613:
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                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-123D20"
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5513. .6417
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239711. .242291
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242342. .243499
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34541. .35596
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site:
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229888. .232421
/note="wgs_end_extensi
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Compugen Ltd.
 version - 2005 (
 GenCore
(c) 1993
         Copyright
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nucleic search, using sw model ı OM nucleic

Run on:

05:48:49 2005, 30, July

updates/sec Search time 270 Seconds (without alignments) 855.074 Million cell up

US-09-667-237B-12 39 Title:

score: Sequence: Perfect

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Gapext 1.0 IDENTITY_NUC Gapop 10.0 , table: Scoring

residues 4390206 seqs, 2959870667 Searched

8780412 of hits satisfying chosen parameters: Total number

08 08 Minimum

seq length: 0 seq length: 200000000 Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqn2003cs: *
geneseqn2003ds: *
geneseqn2004as: *
geneseqn2004bs: * Geneseq_16Dec04:*

geneseqn1980s:*

geneseqn2000s:*

geneseqn2001as:*

geneseqn2001bs:*

geneseqn2002as:*

geneseqn2003as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	h20260 CJ 1	Aa845570 B cell ly	Acd40364 DNA encod	587	7	89	2	739	2788 S	389 Shrimp	Adq97348 Mouse can	362 CJ link	5572 B c	6 DNA enco	Acd06881 Immunogen	Acd06139 Immunogen	Acd45091 DNA encod	Ach32706 Human end	Adf85490 Human ade	Ach89611 Human gen
ΙD	AAH20260	AAS45570	ACD40364	ACD06879	ACD06137	ACD45089	ABD32728	ADG73739	AAH62788	AAH62689	ADQ97348	AAH20262	AAS45572	ACD40366	ACD06881	ACD06139	ACD45091	ACH32706	ADF85490	ACH89611
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ABK45910 ACH7589 AAQ03877 AAS83104 AAQ75166 ADQ9727 AAC31118 AAC31124 AAC31124 AAC31124 AAC31124 AAC31124 AAC31127 AAC31127 AAC31127 AAC31127 AAC31127 AAC3127 AAC3127	ADF816 AAH2026 AAS4557 ACD4036 ACD0688 ACD0614
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ALIGNMENTS

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Polynucleotide library; dual-domain; linker; vaccine; B-cell lymphoma;
                                                                                                           codon given"
                                          CJ linker library oligonucleotide sequence SEQ ID 12
                                                                                    1. .39
/*tag= a
/partial
/product= "Linker"
/note= "No stop or start c
                                                                                 Location/Qualifiers
          ВР
          39
                               (first entry)
          AAH20260 standard; DNA;
                                                                                                                      WO200123543-A1
                                27-JUL-2001
                                                                                                                                 05-APR-2001
                                                                      Synthetic
                    AAH20260;
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RESULT 1
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(LARG-) LARGE SCALE BIOLOGY CORP 99US-0155978P. 2000WO-US025965. 22-SEP-2000; 24-SEP-1999;

Turpen T; Reinl SJ, Lindbo JA, WPI; 2001-316135/33. P-PSDB; AAB97244. Novel library of dual-domain nucleic acid molecules useful for producing dual-domain proteins, or idiotypic scFv vaccine useful for treating B-cell lymphoma.

Example 1; Page 34; 77pp; English.

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Included in
The library
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This invention relates to a library of dual-domain nucleic acid molecules. The two domains in the molecules are separated and linker linker which is a member of a randomised library of linkers. The lir in the library vary in size and nucleotide sequence and consist of a repeated pattern of degenerate repeated triplet nucleotides. Include the invention is a method for the production of the library. The lik is useful for producing dual-domain proteins of interest that have therapeutic value, e.g., idiotypic scFv vaccine for treating B-cell lymphomas. The present sequence represents a linker oligonucleotide sequence generated in an example illustrating the invention. The exactoner the generation of a tumour antigen from a patient that incl the idiotype of CJ B cell lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; B cell lymphoma; cytostatic; immunostimulator; self-antigen; tumour-specific vaccine; tumour; polyclonal immune response; idiotype-specific anti-lymphoma immune response; PCR primer; ss.
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No. 0.0015;
Mismatches
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MCCORMICK A
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P-PSDB; AAU29012.
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   surrace immunoglobulin or a polyclonal immune response to an idiotype. The vaccine composition is useful for inducing a tumour-specific immune antibody response in a tumour-bearing subject or a subject who had a tumour e.g. B-cell lymphoma, and was treated so that no tumour is clinically or radiographically evident. (I) is useful for inducing a protective antitumour immune response. (I) can be produced at high levels, is easy to purify and can be appropriately folded to mimic the conformation of the native epitopes displayed at the tumour cell surface. AAS45529-AAS45579 represent B cell lymphoma self antigen vaccine linker sequences and PCR primers of the invention
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                                                                                                                                                                                                                                                                                                                                             tumour; immunoglobulin V; linker.
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larity 100.0%;
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10-MAR-2000; 2000US-00522900.
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TURPEN T H.
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Best Local Similarity
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surface in
The vaccir
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Best Local
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Mccormick AA,
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                                                    ACD06137;
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                                                                                                                                                                                                                          cytostatic; vaccine;
na-specific vaccine;
ody polypeptide.
 Gaps
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of a
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                                                                                                                                                                                                                         Tumour; immunoglobulin variable region; anti-tumour; cytost; self-antigen; tumour-specific vaccine; B-cell lymphoma-speciB-cell lymphoma; PCR; primer; ss; single chain antibody pol
                                                                                                                                                                                                 single chain antibody polypeptide (scfv) linker
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 Indels
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 Mismatches
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Pred. No.
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10-MAR-2000; 2000US-00522900
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LINDBO J A.
TURPEN T H.
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Matches 39
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 Matches
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The invention describes a polypeptide self-antigen (I) useful as a tumour specific vaccine in a subject with a tumour or at risk of developing a tumour, encoded by a nucleic acid in the cells of the tumour, including an epitope to, or overexpressed by tumour cells; produced in a cell or organism that has been transfected with nucleic acid and in a correctly folded form; and capable of inducing an immune response in a mammal. (I) is useful as a tumour-specific vaccine, especially a B-cell lymphoma. Specific immune antibody response in a tumour-bearing subject, preferably human or a subject who had a tumour and was treated so that no tumour is clinically or radiographically evident, where the tumour is B-cell lymphoma. This sequence encodes a linker peptide associated with single chain antibody polypeptides which function to join the variable heavy and variable light chain encoding DNA's together forming the single chain
                                                                                                                                                                                                      Tumour; immunoglobulin variable region; anti-tumour; cytostatic; vaccine; inducer of immune response; self-antigen; B-cell lymphoma; tumour-specific vaccine; single chain antibody polypeptide; linker; ds.
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                                                                                                                                                        Immunogenic single chain antibody polypeptide (scfv) linker DNA
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ACD06137 standard; DNA;
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LINDBO J A.
TURPEN T H.
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TUSE D.
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P-PSDB; ABO01257.
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The invention describes a polypeptide self-antigen (I) useful as tumour-
specific vaccine in subject with a tumour, including an epitope or
epitope unique to, or overexpressed by, cells of the tumour, is produced
in a cell or organism that has been transformed or transfected with the
nucleic acid derived from the tumour of subject, and is capable of
inducing an immune response in a mammal without a need for adjuvant or
other immunostimulatory materials. (I) is useful for inducing an immune
cesponse, preferably a protective anti-tumour immune response in a
mammal, preferably human. A vaccine composition comprising (I) is useful
for inducing a tumour-specific immune antibody response in a tumour-
bearing subject (preferably human) or a subject who had a tumour and was
treated so that no tumour is clinically radiographically evident. The
vaccines are preferably useful for inducing immune antibody response
cagainst B-cell lymphoma. The polypeptide is produced without the need for
denaturation or renaturation. (I) is rapidly produced in plants by
transient viral expression. Plant samples expressing the desired protein
can be positively identified by both enzyme linked immunosorbent assay
(ELISA) and Western blotting 4 weeks after molecular cloning. Thus, (I)
is expressed rapidly and easily in plants. This sequence encodes a self-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide antigen which includes epitope overexpressede.g. B-cell lymphoma, and is capable of inducing immune without need for adjuvant, useful as anti-tumor vaccine
                                                                          Self-antigen; tumour-specific vaccine; tumour; immune respon
anti-tumour immune response; vaccine; B-cell lymphoma;
transient viral expression; transgenic plant;
variable region gene fragment; linker; ds.
                                                  peptide
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                                                 vaccine associated linker
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10-MAR-2000; 2000US-00522900.
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antigen associated linker
                                                self-antigen
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TURPEN T H
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                  10-SEP-2003
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                                                                                                                                                                     Synthetic
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 Length 39;
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Score 39; DB 9;
Pred. No. 0.0015;
Mismatches
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ABD32728 standard; DNA; 109453

RESULT 7 ABD32728 ID ABD3

Query Match

Length 109453;

DB 13;

Score 30;

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The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above comprising at least one probe comprising at least to encoded within a cancer-associated (CA) nucleic acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above—mentioned nucleotide sequences, an isolated polypeptide (encoded within an open reading frame of a CA sequence selected from any of the 95 complement), an isolated antibody, for its antigen binding fragment) that compoclonal antibody, a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical composition comprising cancer cells (comprising the antibody cited above, methods for diagnosing cancer cells (comprising the antibody cited above, methods for diagnosing cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, an electronic library comprising the above polypeptide (or their fragments), methods of screening the articancer activity of a CA protein (CAP), methods for detecting cancer cells in an individual and contracting cancer cells associated with expression of a polypeptide in a test cell sample, and method for treating cancer and method for individual and m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA gene in a cell. The composition and methods are useful for detecting, diagnosing, preventing and treating cancers, especially lymphoma and leukaemia. These may also be used in screening for agents that modulate cancer. The present sequence is a mouse CAP genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma an leukemia, or in screening for agents that modulate cancer.
                                                                                                                                                          cytostatic;
                                                                                                             cancer-associated genomic DNA MD15-016
                                                                                                                                                    cancer-associated protein; gene; lymphoma; CAP.
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2003US-00388838.
2003US-00417375.
2003US-00461862.
2003US-00663431.
2003US-00737318.
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15-APR-2003;
13-JUN-2003;
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15-DEC-2003;
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leukaemia;
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a sequence that is differentially expressed in a native fungus exhibiting a filamentous morphology relative to the native fungus exhibiting a filamentous morphology. The method also comprises: providing a recombinant polynucleotide comprising an antisense orientated sequence that is complementary to at least part of a gene; transforming a fungus with the recombinant polynucleotide; and suppressing expression of the gene utilising transcription products produced by expression of the recombinant polynucleotide, the suppression promoting the morphology. The polynucleotide is useful for promoting morphology in a fungus and enhancing a bioprocess such as expressing cellulase, expressing lignase, converting biomass to alcohol, producing organic acids, producing peptic enzyme or fumaric acid or producing lovastatin. This sequence represents Aspergillus niger Brsa-109 converting is differentially expressed in the pellet morphology relative to the filamentous morphology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a new isolated polynucleotide molecule comprising
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gillus niger Brsa-109
morphology relative
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                                                                                                                                                                                                                                                                                        differential gene expression; fungus; pellet morphology; filamentous morphology; gene suppression; bioprocess; cellulase expression; hemicellulase expression; lignase expression; biomass conversion; organic acid production; peptic enzyme production; fumaric acid production; lovastatin production; Brsa-109; gene; ss.
                   Gaps
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Pred. No. 3.7;
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   ed. No. 2.4 Mismatches
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   Pred.
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ilarity 86.5%;
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86.8%;
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l Similarity
33; Conserv
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P-PSDB; ADG73740
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Matches
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The invention provides the primary nucleotide sequence of the WSBV genome (AAH62689), predicted transcript sequences (AAH626899-AAH62839) and encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create transgenic viral resistant shrimp. (Updated on 06-AUG-2003 to correct OS
                                                                                                                                   viral infection;
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Pred. No. 3.9;
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ilarity 86.5%;
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P-PSDB; AAG85008.
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Best Local Similarity
Matches 32; Conser
                                                                                                                                                                                   Shrimp white spot
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11-SEP-2001
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ID AAH62689
              2788/c
AAH62788
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The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                         nucleic acids comprising at least for diagnosing, preventing and/or
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22-DEC-2003; 2003WO-US041389
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31; Conservative
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                                                   Shrimp white spot Bacilliform virus; WSBV; diagnosis; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp; ds.
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                          Bacilliform virus (WSBV)
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SINOGENOMAX CO LTD.
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ADQ97348 standard; DNA;
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11-SEP-2001
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Novel library of dual-domain nucleic acid molecules useful for producing dual-domain proteins, or idiotypic scFv vaccine useful for treating B-

WPI; 2001-316135/33 P-PSDB; AAB97231.

WO2004060304-A2

ADQ97348;

ADQ97. ESUL

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Mouse

Query Match

field.)

Local

Matches Best

22-JUL-2004

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Gaps

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92520

B-cell lymphoma;

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55510 T;

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Xu X,

WPI;

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Length 204803;

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                                          This invention relates to a library of dual-domain nucleic acid molecules. The two domains in the molecules are separated and linkers linkers. The two domains in the molecules are separated and linkers in the library of linkers. The linkers in the library vary in size and nucleotide sequence and consist of a repeated pattern of degenerate repeated triplet nucleotides. Included in the invention is a method for the production of the library. The library is useful for producing dual-domain proteins of interest that have therapeutic value, e.g., idiotypic scFv vaccine for treating B-cell lymphomas. The present sequence represents a linker oligonucleotide sequence generated in an example illustrating the invention. The example concerns the generation of a tumour antigen from a patient that includes the idiotype of CJ B cell lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ing the tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an
cells
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sk of
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel polypeptide self-antigen (I) useful tumour-specific vaccine in a subject with a tumour or at risk of developing a tumour. (I) includes an epitope or epitopes unique to, over expressed by, cells of the tumour, thereby distinguishing the term all other tumours of the same or different histological type, of the subject or in another member of the subject's species. (I) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; B cell lymphoma; cytostatic; immunostimulator; self-antigen; tumour-specific vaccine; tumour; polyclonal immune response; idiotype-specific anti-lymphoma immune response; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptide vaccine produced in plants, useful for inducing immune response to a self-antigen on the surface of certain tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                          cell lymphoma CJ linker library, linker nucleotide sequence
                                                                                                                                                                                                                                  Length 39;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                          T; 0 U; 0 Other;
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Pred. No. 4.3;
                                                                                                                                                                                                                                                                                           ed. No. 4.3 Mismatches
                                                                                                                                                                                                          G; 13
                     Example 1; Page 34; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Page 59; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORP
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                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                          6 A; 7 C; 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-2000; 2000WO-US028362
                                                                                                                                                                                                                                72.8%;
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A.
                                                                                                                                                                                                                                                                                                                                                                   AAS45572 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LARGE SCALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-596903/67
                                                                                                                                                                                                                                           Similarity 32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide
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                                                                                                                                                                                                          Sequence 39 BP;
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cell lymphoma.
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Matches
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                                                                                                                                                                                                                                                                                                                                           RESULT
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epitopes in their native form. (I) is capable of inducing an immune response in a mammal, when used as an individual-specific immunogenic product comprising (I); and as a vaccine composition useful for inducing a tumour-specific immune response, idiotype-specific anti-lymphoma immune response, a polyclonal immune response to at least one idiotype of a surface immunoglobulin or a polyclonal immune response to an idiotype. The vaccine composition is useful for inducing a tumour-specific immune antibody response in a tumour-bearing subject or a subject who had a tumour e.g. B-cell lymphoma, and was treated so that no tumour is clinically or radiographically evident. (I) is useful for inducing a protective antitumour immune response. (I) can be produced at high conformation of the native epitopes displayed at the tumour cell surface.

AAS45529-AAS4559 represent B cell lymphoma self antigen vaccine linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene; ds; gene therapy; vaccine; tumour; immunoglobulin V; IgV; CJ heavy chain; variable region; linker.
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                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                              1.4; DH
                                                                                                                                                                                                                                                                                                                                                                                                                                      ed. No. 4.3
                                                                                                                                                                                                                                                                                                                           sequences and PCR primers of the invention
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2000US-00522900
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st Local Similarity 84.2%;
tches 32; Conservative
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TURPEN T H
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10-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              more epitopes of antigen
                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour; immunoglobulin variable region; anti-tumour; cytosta
self-antigen; tumour-specific vaccine; B-cell lymphoma-speci
B-cell lymphoma; single chain antibody polypeptide; scfv; ds
                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic single chain antibody polypeptide (scfv) linker
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7 C; 13 G; 13 T; 0 U; 0 Other;
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mammals, is produced in plants and mimics one or
uniquely expressed by cells of tumor.
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                                                                                                                                CTACTGCTACTGGTGCTAGTACTACTGCTGGTGCTAGT
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                                           DB
                                         Score 28.4; DB Pred. No. 4.3; 0; Mismatches
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2000US-00522900.
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84.2%;
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REINL S J.
LINDBO J A.
TURPEN T H.
                                                                Similarity
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39 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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10-MAR-2000;
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                                                                                  32;
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 Sequence
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Best Local
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(REIN/)
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Gaps

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Indels

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Conservative

Local Similarity

Query Match

32;

Best Loc Matches

Length 39;

6;

DB

Score 28.4; Di Pred. No. 4.3; Mismatches

72.8%;

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NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3376 base pairs
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29, Appl
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3, Appli
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Seq
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-545-860D-29

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US-07-973-431B-2

US-09-181-585-3

US-09-181-585-1

US-09-949-016-189405

US-09-949-016-189409

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US-09-949-016-189409

US-09-949-016-189409

US-09-949-016-189409

US-09-949-016-18578

US-09-949-016-14578

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MATION:
Croce, Carlo
Canaani, Eli
Canaani, Eli
VENTION: Diagnostics, Therapeutics and Methods
VENTION: for Detection and Treatment of Acute Leukemias
VENTION: For Detection and Treatment of Acute Leukemias
VENTION: Resulting from Chromosome Abnormalities in the All-1
TOTAL SESSIBLE SESSIBLE OF THE SES
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APPLICATION NUMBER: PCT/US94/n/1.25
FILING DATE:
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                     TJU-1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US94-04496-29/c; Sequence 29, Application PC/TUS9404496; GENERAL INFORMATION:
                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3376 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Philadelphia
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 29
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: double
                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 82.
32; Conservative
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                                                                                                                                                                                                                                                                                                                                                      CDS
196..1902
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LOCATION: 196..1902
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STREET: On
CITY: Phil
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US-08-545-860D-29/C
SEQUENCE 29, Application US/08545860D
Fatent No. 6040104
Fatent No. 6040104
Fatent No. 6040104
FAPLICANT: Canaal, Ell
FILE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-
NUMBER OF SEQUENCES:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
ADPLICATION NUMBER: US/08/545,860D
FILING DATE: US/08/545,860D
FILING DATE: DO-MAR-1994
FRIOR APPLICATION NUMBER: DET/US92/10930
FILING DATE: PCT/US92/10930
FILING DATE: DS-C-1994
FRIOR APPLICATION DATA: PCT/US92/10930
FILING DATE: 19-0CT-1994
FRIOR APPLICATION DATA: WAPLICATION DATA: APPLICATION NUMBER: US/08/546; SP
FILING DATE: 11-0CT-1994
FRIOR APPLICATION DATA: WAPLICATION DATA: APPLICATION DATA: WAPLICATION DATA: WAPLICATION DATA: WAPLICATION DATA: WAPLICATION DATA: WAPLICATION DATA: WAPLICATION NUMBER: US/08/062.443
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ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,229
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
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STRANDEDNESS: double TOPOLOGY: line
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LOCATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-181-585-1
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US-09-181-585-3
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LENGTH: 1471
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; Sequence 3, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF ;
; FILE REFERENCE: 11000900101
; FILE REFERENCE: 1900900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
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                                                  US-07-973-431B-2/c

Sequence 2, Application US/07973431B

Patent No. 5652144

GENERAL INFORMATION:

APPLICANT: Lu, Yinchen

APPLICANT: Haseltine, William A

TITLE OF INVENTION: YC1 Protein, Gene, And Uses The

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: David G. Conlin; Dike, Bronstein,

ADDRESSEE: Roberts & Cushman

STREET: 130 Water Street

CITY: Boston

STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/973,431B
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Pred. No. 3.1;
0; Mismatches
Mismatches
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41968
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-6440
TELEPHONE: (617) 523-6440
TELEFAX: (617) 523-6440
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Best Local Similarity 81.6%;
Matches 31; Conservative
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LENGTH: 1534 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
Conservative
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US-09-181-585-1
; Sequence 1, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 11000900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1159
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; Sequence 2, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 11000900101
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Description of Artificial comprising exons E, C, an
                                                        Score 26.4; D. Pred. No. 4; 0; Mismatches
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Mismatches
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Pred. No. 4
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CURRENT FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
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illarity 83.3%;
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Similarity 83.3%;
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ASSOCIATED
OF DETECTION AND USES THEREOF
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 189407
LENGTH: 601
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES FILE REFERENCE: CL001307
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US-09-949-016-189409/c
; Sequence 189409, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: Fast SEQ for Windows Version 4.0
SEQ ID NO 189408
LENGTH: 601
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Similarity 79.5%;
31; Conservative
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Matches 31; Conser
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; ORGANISM: Human
US-09-949-016-189408
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                                                                                  Sequence 189405, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03
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Pred. No. 4.4;
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08
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Pred. No. 4
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SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version
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llarity 79.5%;
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Similarity 79.5%;
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Matches 31; Conser
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S-09-949-016-189407/c
                                                                      -09-949-016-189405/c
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US-09-949-016-189406
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LENGTH: 601
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LENGTH: 601
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Sequence 14577, Application US/09949016

Sequence 14577, Application US/09949016

Patent No. 6812339

Patent No. 6812309

Patent No. 6812309

TITLE OF INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14577

LENGTH: 678533
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Pred. No. 12;
0; Mismatches
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Mismatches
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17163
LENGTH: 92074
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Best Local Similarity 79.5%;
Matches 31; Conservative
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Best Local Similarity
Matches 31; Conser
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US-09-949-016-14577/c
                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17163
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
** PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 7819
LENGTH: 825
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; Sequence 17163, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,768
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 189409
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| cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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, Stephen O, John N, Thomas N: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER 8696-169195 NUMBER: US/09/539,382 TE: 2000-03-10 NUMBER: US 60/155,579 : 1999-09-24 NOS: 62 n version 3.0 n eature N: linker	; APP	LICANT:	TUSE, D	aniel					
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N, Thomas N: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER 8696-169195 8696-169195 ON NUMBER: US/09/539,382 TE: 2000-03-10 NUMBER: US 60/155,579 1999-09-24 NOS: 62 In version 3.0	; APP	LICANT:	LINDBO,	John					
N: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER 8696-169195 ON NUMBER: US/09/539,382 ON NUMBER: US 60/155,579 TE: 2000-03-10 NUMBER: US 60/155,579 I 1999-09-24 IN Version 3.0	, APP	LICANT:	TURPEN,	Thomas					
8696-169195 ON NUMBER: US/09/539,38 TE: 2000-03-10 NUMBER: US 60/155,579 : 1999-09-24 NOS: 62 n version 3.0 n eature N: linker	; TIT	LE OF IN	VENTION:	SELF A	NTIG	VACCINES FOR TREATING	CELL	AND	
ON NUMBER: US/09/539,38 TE: 2000-03-10 NUMBER: US 60/155,579 : 1999-09-24 NOS: 62 n version 3.0 n n N: linker	FIL	E REFERE	NCE: 186	96-1691	92				
TE: 2000-03-10 NUMBER: US 60/155,57 : 1999-09-24 NOS: 62 n version 3.0 n eature N: linker	, GUR	RENT APP	LICATION	NUMBER	: US	/09/539,38			
NUMBER: US 60/155,57: 1999-09-24 NOS: 62 n version 3.0 n eature N: linker	. CUR	RENT FIL	ING DATE	2000	-03-	10			
: 1999-09-24 NOS: 62 n version 3. n eature N: linker	, PRI	OR APPLI	CATION N	UMBER:	us 6	0/155,57			
NOS: 62 n version 3. n eature N: linker	, PRI	OR FILIN	G DATE:	1999-09	-24				
n n eature N: linker	EOZ C	BER OF S	EQ ID NO	S: 62	,				
LENGTH: 39 TYPE: DNA CORGANISM: Unknown FEATURE: NAME/KEY: misc feature LOCATION: ()() COTHER INFORMATION: linker US-09-539-382-45	 	TWAKE: P	acentin	version	າ ວ				
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n eature N: linke	3 2	אנועם ישנו פועם ישנו							
FEATURE: NAME/KEY: misc feature LOCATION: ()() OTHER INFORMATION: linke		PE: DNA	Tribroum						
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LOCATION: ()() OTHER INFORMATION: linke	AN	ME/KEY:	44	ture					
OTHER INFORMATION: linke -09-539-382-45	3	CATION:		i					
-09-539-382		HER INFO	NOI	linke					
	-	539-382-	45						

Length 39;

DB 10; 0.00029;

Score 39; Pred. No.

100.0%;

Query Match Best Local Similarity

o

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WS-10-067-893-45

i Sequence 45, Application US/10067893

j Publication No. US20030044420A1

j GENERAL INFORMATION:

j APPLICANT: MCCORMICA, Alison

j APPLICANT: TUSE, Daniel

j APPLICANT: TURE, Daniel

j APPLICANT: TUREN, Thomas

j TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CAN(

j FILE REFERENCE: 18696-169194

j CURRENT APPLICATION NUMBER: US/10/067,893

j CURRENT PILING DATE: 2002-02-08

j PRIOR APPLICATION NUMBER: US 60/155,579

j PRIOR FILING DATE: 1999-09-24

j NUMBER OF SEQ ID NOS: 62

j SOFTWARE: PATENTIN VERSION 3.0
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APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer;
FILE REFERENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/388,838
CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81
TYPE: DNA
CORGANISM: Mus musculus
US-10-388-838-81
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Pred. No. 0.00029;
Mismatches 0;
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                              Score 39; DB 14;
Pred. No. 0.00029
Mismatches 0
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Pred. No. 1.4;
0; Mismatches
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larity 86.8%;
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39; Conservative
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ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
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Matches 39; Conser
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US-10-388-838-81
 US-10-067-892-45
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LENGTH: 39
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i Sequence 45, Application US/10067892

j Publication No. US20030039659A1

i GENERAL INFORMATION:

APPLICANT: MCCORMICK, Alison

APPLICANT: TURE, Daniel

APPLICANT: TURPEN, Stephen

APPLICANT: TURPEN, Thomas

TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYM

TITLE OF INVENTION: AND OTHER CANCERS

FILE REFERENCE: 18696-169194

CURRENT APPLICATION NUMBER: US/10/067,892

CURRENT APPLICATION NUMBER: US/09/522,900

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.0

SEQ ID NO 45

LENGTH: 39
                                                                                                                                                                                           APPLICANT: MCCORMICK, Alison
APPLICANT: MCCORMICK, Alison
APPLICANT: TUSE, Daniel
APPLICANT: TUSE, Daniel
APPLICANT: LINDBO, John
APPLICANT: LINDBO, John
APPLICANT: LINDBO, John
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYM
FILE REFERENCE: 18696-169194
CURRENT APPLICATION NUMBER: US/10/067,790
CURRENT FILING DATE: 2002-02-08
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.0
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100.0%; Pred. No. 0.00029;
tive 0; Mismatches 0;
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39; Conservative
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; LOCATION: ()..()
; OTHER INFORMATION: linker
US-10-067-790-45
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NAME/KEY: misc feature
LOCATION: ()..()
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39;
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LENGTH: 39
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GENETIC POLYMORPHISMS ASSOCIATED WITH
                    Length
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               DB 2
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US-10-719-993-1903/c
; Sequence 1903, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, MET;
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1903
; LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-719-993-1907/c

Sequence 1907, Application US/10719993

Publication No. US20040265849A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS AS:

TITLE OF INVENTION: ALZHEIMER'S DISEASE, ME:

FILE REFERENCE: CL001496

CURRENT APPLICATION NUMBER: US/10/719,993
                                                          Mismatches
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Pred. No.
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; Sequence 10972, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1907
LENGTH: 201
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US-10-719-993-1903
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APPLICANT: INOKO, Hidetoshi

APPLICANT: TAMIYA, Gen

TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS

FILE REFERENCE: ORIN-003CIP

CURRENT APPLICATION NUMBER: US/10/674,124A

CURRENT FILING DATE: 2003-09-26

PRIOR APPLICATION NUMBER: 10/257,511

PRIOR FILING DATE: 2000-10-30

PRIOR PPLING DATE: 2000-10-30

PRIOR PPLING DATE: 2000-10-30

PRIOR FILING DATE: 2000-4-13

PRIOR FILING DATE: 2000-04-13

PRIOR FILING DATE: 2002-09-28

PRIOR PPLING DATE: 2002-09-28

PRIOR PILING DATE: 2002-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19
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22948 CTGCTGCTGGTGCTAGTACTGCTGGTGGTGCTAGT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39
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Pred. No. 0.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
TITLE OF INVENTION: ALZHEIMER'S DISEASE, ME
FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Located on chromosome FEATURE:
                                                                                                               US-10-674-124A-10191/c; Sequence 10191, Application US/10674124A; Publication No. US20040197797A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-719-993-1896/c
; Sequence 1896, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: DISO7_10002156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 84.6%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 27110
SEQ ID NO 10191
LENGTH: 192
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                                                                                                                                                                            GENERAL INFORMATION:
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LENGTH: 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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Gaps

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Indels

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Mismatches

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Sequence 95, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                   ACTACTGCTACTGGTGCTAGTACTACTGCTGGTGCTAGT
                                                  ACTACTGCTACTGGTGCTAGTACTACTGCTGGTGCTAGT
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Pred. No. 1.7;
1; Mismatches
  Pred. No.
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82.1%;
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Similarity 82.1%;
32; Conservative
82.1%;
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                 Conservative
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; ORGANISM: Homo sapiens
US-10-719-993-96
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Best Local Similarity
Matches 32; Conser
                                                                                                                                                   -10-719-993-95/c
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SEQ ID NO 95
LENGTH: 3261
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SEQ ID NO 96
LENGTH: 3637
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US-10-719-993-95
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Best Local S
Matches 32
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Best Local S
Matches 32
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 ALZHEIMER'S DISEASE, METHODS OF DETECTION
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                                                                                                                                                                                                      Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lasure, Linda L.
APPLICANT: Lasure, Linda L.
APPLICANT: Dai, Ziyu
TITLE OF INVENTION: Isolated Polynucleotides and Methods of
TITLE OF INVENTION: a Fungus
FILE REFERENCE: BA4-195
CURRENT APPLICATION NUMBER: US/10/442,017
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: 60\382,132
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 37
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Pred. No. 1.6;
0; Mismatches
                                                                                                                                                                                                     Score 29; DB 2
Pred. No. 1.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/10719993;
Publication No. US20040265849A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS;
TITLE OF INVENTION: ALZHEIMER'S DISEASE, ME;
FILE REFERENCE: CL001496
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 3179
            FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10972
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/10442017
Publication No. US20030215950A1
GENERAL INFORMATION:
APPLICANT: Battelle Memorial Institute
APPLICANT: Lasure, Linda L.
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ilarity 86.5%;
Conservative (
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                                                                                                                                                                                                   Similarity 82.1%; 32; Conservative
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US-10-442-017-16
                                                                                                                                                     sapiens
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 TITLE OF INVENTION:
                                                                                                                                                 ; ORGANISM: Homo US-10-719-993-10972
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US-10-719-993-97
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US-10-442-017-16/c
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Best Local
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Gaps

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Indels

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Length 3261;

20;

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US-10-719-993-6780/c
US-10-719-993-6780/c
; Sequence 6780, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
                                                                          APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACTGCTACTGGTGCTAGTACTACTGCTGGTGCTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
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Pred. No. 1.8;
1; Mismatches
Sequence 96, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
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Length 3179;

DB 20;

Score 29;

74.48;

Query Match

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; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFT DATE: 289730
; SEQ ID NO 6780
; TYPE: DNA
; OGGANISM: Homo sapiens
; CRGANISM: Homo sapiens
; CRGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(289730)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1. US-10-719-993-6780

OURLY MATCH

Watches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

A ATTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 214221

Db 214259 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTACTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC
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Search completed: July 30, 2005, 08:24:04 Job time : 416 secs This Page Blank (uspto)

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                    Copyright
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- nucleic search, using sw model OM nucleic July 30, 2005, 06:59:54; Search time 2067 Seconds (without alignments) 718.194 Million cell updates/sec Run on:

US-09-667-237B-12 Title: Perfect score: Sequence:

1 actactgctactggtgctagtactactgctggtgctagt

39

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

residues 34239544 seqs, 19032134700 Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: * Database

gb_est1:*
gb_est2:*
gb_est3:*
gb_est4:*
gb_est5:*
gb_est6:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ф			SUMMAKIES	
0.	Score	Ouery Match		DB	ΩI	Description
	33.	86.7	10		0219	AL014813 F.ru
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ហ		9	S	σ	01369	04939 F.rubri
v	30	9	Ø	Φ	4339	43398 OGAOW57
7		ç.	σ	,	3193	31932 AL93193
ω		76.9	4	ω	4341	43413 OGAOW57
σ		75.4		σ	FR0021848	rip
	9.	75.4	S	თ	0268	19712 F.rubrip
	<u>د</u>	75.4	0	ω	8379	83794 PUBCV45
	<u>.</u>	75.4	5	σ	0184	11359 F.rubrip
	9	75.4	5	Φ	3472	34726 RPCI-23-
	φ.	75.4	N	σ	03CM	37969 Te
15	29.4	75.4	m	σ	4 N	99119 Tetra
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	ъ Э	2	Ŋ	N	7983	E679837 df57a0
	28.4	ς.		σ	FR0026865	69

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Gaps

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Indels

Query Match
Best Local Similarity 89.7%; Pred. No. 0.078;
Matches 35; Conservative 0; Mismatches 4;

Length 410;

P190034 BP190	Z90761 F.rubripes	444208 Fugu ru	661564 BJ6615	49626 BJ64962	304427 Tetraodo	843342 OR_CBa00	8114 ZMMBBb	900918 ZMMBBb05	687985 nbxb0076	784725 fzmb013f	589218 tigr-gss	012413 F. rubrip	251992 EST01792	126074 60315135	763893 BMBAC314	M627819 17000687	12474 daa18e10	U126727 6031509	126090 60315034	F612625 daa19h0
P19003	FR0006951	R00474	156	J64962	NS04RW	34334	8811	90091	58798	78472	21	00195	25199	12607	76389	M62781	F61247	12672	U12609	1262
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ALIGNMENTS

FR0021942 F. rubripes GSS sequence, clone 070F18aB11, genomic survey sequence. AL014813 AL014813.1 GI:2681181 GSS; genome survey sequence. Takifugu rubripes (Fugu rubripes)	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostei, Actinopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetradontoidea, Tetraodontidae, Takifugu. Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.J., Bouchireb, N., Cottage, A., Yeo, G.S., Umrania, Y., Williams, G. and	Į.	Eigar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S. Direct Submission Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk Vector: pBluescript II KS V type: phagemid PRIMER: KS	Descritions of cosmid cloned genomic sequencing of cosmid cloned genomic sequence. Location/Qualifiers 1410 /organism="Takifugu rubripes" /mol_type="genomic DNA" /db_xref="taxon:31033" /clone="070F18aB11"
FRO021942/c LOCUS DEFINITION F. r ACCESSION ALO VERSION ALO KEYWORDS GSS SOURCE TAK	•	_	TITLE Direct JOURNAL Submit COMMENT Vector V type	DESCK: One passequensearth

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

RESULT 2 BZ423698

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280 bp DNA linear GSS 25-FEB-2004 clone 031C10aF9, genomic survey sequence.
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Direct Submission
Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
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Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
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AL012412
AL012412.1
GI:2678780
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
 Tetraodontiformes
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Bouchireb, N., Cottage, A., Yeo, G.S., Umrania, Y., Williams, G. a
                                                                          Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.
Bouchireb, N., Cottage, A., Yeo, G.S., Umrania, Y., Williams, G. a
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontoidea; Tetraodontidae; Takifugu.
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Pred. No. 0.81;
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Generation and analysis of 25 Mb of Fugu rubripes by sequence scanning Genome Res. 9 (10), 960-971 (1999) 99455097
                                                                                                                                                     of 25 Mb of
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/db_xref="taxon:31033"
/clone="133B16aC7"
/clone_lib="cosmid 133B16"
                                                                                                                       Brenner, S.
Generation and analysis of 25 Mb of
Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
99455097
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Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

E 1 (basea 1 to 513)

S Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A.

Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)

L Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8884
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/lab_host="DH5a"
/clone lib="WGS-SbicolorF (DH5a methyl filtered)"
/clone lib="WGS-SbicolorF (DH5a methyl filtered)"
/note="Site_1: Xba I; Site_2: Xba I; The vector was
digested with XbaI and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (.x/y reads in M13mpl9,
.b/g reads in pUC19). The same ligation was transformed
into DH5a."
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Neoteleostei;
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1; Poales; Poaceae; PACCAD
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id52c10.gl WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor genomic clone id52c10 5', genomic survey sequence.
BZ423698
BZ423698.1 GI:26373196
GSS.
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F.rubripes GSS sequence, clone 133B16aC7, genomic sur 290754.1 GI:1867968
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei;
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0.8;
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/mol_type="genomic DNA"
/db_xref="taxon:4558"
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Similarity 87.2%;
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FEATURES

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from the pufferfish

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Query Match Best Local S Matches 34

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DEFINITION ACCESSION

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LOCUS

KEYWORDS SOURCE ORGANISM

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us-09-667-237b-12

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FEATURES

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BZ643398
OGAOW57TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0111J17, genomic survey sequence.

BZ643398
BZ643398
BZ643398.1 GI:28104877
GSS.
Zea mays
SM Zea mays
SM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

E 1 (bases 1 to 480)
S Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
L Unpublished (2002)
Other_GSSs: OGAOW57TM
Contact: Cathy Whitelaw
              bp DNA linear GSS 29-JAN-2003 mays genomic clone ZMMBMa0111J17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Christophides, G.K., Blass, K., Zdobnov, E.M., Carmouche, R., Benes, and Kafatos, F.C.
Anopheles gambiae EST, European Molecular Biology Laboratory
Unpublished (2002)
Contact: Christophides GK
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany
Tel: +49 6221 387-440
Fax: +49 6221 387-306
Email: christop@embl-heidelberg.de
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Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL931932
AL931932 NAP1 Anopheles gambiae cDNA clone NAP1-P87-E-03-5,
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/organism="Zea mays"
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/clone="ZMMBMa0111J17"
/clone lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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ON F.rubripes GSS sequence, clone 133B16cD1, gencm...
N AL004939
AL004939
AL004939.1 GI:2450509
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
Actinopterygii; Tetraodontidae; Takifugu.
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                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-SEP-1997) MRC Human Genome Mapping Proj
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@h
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
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                                                                                                                                                                                                     Length 280;
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/mol_type="genomic DNA"
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/clone="133B16cD1"
/clone_lib="cosmid 133B16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, S., Meek, S.,
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                                                                    /organism="Takifugu rubripes/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="031C10aF9"
/clone_lib="cosmid 031C10"
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   sequencing
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Pred. No. 1
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Elgar, G., Clark, M., Smith
Williams, G. and Brenner, S
Direct Submission
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ilarity 84.6%;
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REFERENCE AUTHORS

JOURNAL

COMMENT

JOURNAL MEDLINE

TITLE

- PUBMED

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Benes, V.

Local

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FEATURES

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Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y. Bouchireb, N., Cottage, A., Yeo, G.S., Umrania, Y., Williams, G. a
   CTACTGCTACTGCTAGTACTACTGCTGGTGCTAGT
                                                                                                                  F.rubripes GSS sequence, AL014719
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

L (bases 1 to 843)
S Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Consortium for Maize Genomics
L Unpublished (2002)
Other_GSS: OGAOWS7TC
Contact: Cathy Whitelaw
                                        /mol_type="mRNA"
/db_xref="taxon:7165"
/db_xref="taxon:7165"
/clone="NAP1-P87-E-03-5"
/lab_host="E. coli DH10B"
/clone lib="NAP1"
/note="Vector: pT7T3D-Pac (Pharmacia); Site 1: NotI;
Site_2: EcoRI; ESTS sequenced from the T7 priming site that reads from the 5' end of cDNA. The NAP1 is a directionally cloned and normalized, oligo-T primed cDNA library constructed from a mixture of Anopheles gambiae developmental stages according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
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OGAOW57TM ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0111J17, genomic survey sequence.
BZ643413
BZ643413.1 GI:28104915
GSS.
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Fax: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 843
/mol_type="genomic DNA"
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/clone="ZMMBMa0111J17"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site 1: H
methylation filtered genomic DNA
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ilarity 86.8%;
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genomic DNA from the pufferfish
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Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
                                                                                                                                                                                     AL014719.1 GI:2681087
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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and
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F.rubripes GSS sequence, clone 181A
AL019712
AL019712.1 GI:2686080
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
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Pred. No. 2
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GSS 25-FEB-2004 survey sequence.

from the pufferfish

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21-DEC-1999

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2 (bases 1 to 470)
Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y.,
Williams, G. and Brenner, S.
Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
Submitted (08-DEC-1997) ARC Human Genome Mapping Project Resource
                                                                                                                                                                                                                   FR0018463
F. rubripes GSS sequence, clone 016E10aC6, genomic survey sequence.
AL011359
AL011359.1 GI:2676793
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                          Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.J. Bouchireb, N., Cottage, A., Yeo, G.S., Umrania, Y., Williams, G. and Brenner, S.
Generation and analysis of 25 Mb of genomic DNA from the puffer! Fugu rubripes by sequence scanning Genome Res. 9 (10), 960-971 (1999)
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RPCI-23-290D23.TV RPCI-23 Mus musculus genomic clone RPCI-23-290D23, genomic survey sequence.
AQ934726
AQ934726.1 GI:6623740
GSS.
Mus musculus (house mouse)
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/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
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/clone_lib="cosmid 016E10"
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Pred. No. 2.9;
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Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
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                                           Similarity 84.6%;
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PUBCV45TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa026G18,
genomic survey sequence.
BZ683794.1 GI:28241439
GSS.
Zea mays
SM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

I (bases 1 to 307)
SM Xea mays
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

I (bases 1 to 307)
SW Hitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy Whitelaw
                             pufferfish
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veneration and analysis of 25 Mb of genomic DNA from the
Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
10523524
2 (bases 1 to 257)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranie
Williams,G. and Brenner,S.
Direct Submission
L Submitted (08-DEC-1997) MRC Human Genome Mapping Project Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared
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/clone="ZMMBTa026G18"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector:_pCR4-TOPO; Site_1:
CoT_selected_genomic_DNA_library"
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/mol_type="genomic DNA"
/db_xref="taxon:31033"
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/clone_lib="cosmid 181A15"
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One pass dye-terminator sequencing of
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/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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                                                                                                                                                         Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 290 row: D column: 23
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney_and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
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                                    Murinae; Mus
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                 Euteleostomi;
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AL237969
AL237969.1 GI:7897104
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
                                                                                         Krol, M.,
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                                                                          Shatsman, S
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                                                                                         Geer, K.
ыкагуота; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 472)
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                                                                                   Akinret, B., Levins, M., Mcgann, S., Tsegaye, G. Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-290D23"
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                                                                     Feldblyum, T., .. Mcgann, S., ?
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Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

Submitted (12-APR-2000) Genoscope - Centre National de Sequencas.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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GSS; genome survey sequence.
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Actinopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                  Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F. Saurin, W., Bernot, A. and Weissenbach, J.
Characterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation any not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names (Zhirong Bao and Sean Eddy, submitted), and those beginning 'Dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                        http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-10316
is from a CHORI-211 BAC library
VECTOR: pTARBAC2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

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Contact: zfish-help@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
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                      Reinl, S.J., Lindbo, J.A. and Turpen, T. Creation of variable length and sequer dual-domain or multi-domain molecules Patent: WO 0123543-A 12 05-APR-2001; Large Scale Biology Corporation (US)
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